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11050 U.S. PTO
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10 30 50
 CACGCGTCCGCGGGCGCGGCCGGAGAACCCCGCAATCTTTGCGCCCACAAAATACACCGA
 70 90 110
 CGATGCCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
 130 150 170
 CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGGCCCGGAAAAGG
M E O R G O N A P A A S G A R K R
 190 210 230
 CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T
 250 270 290
 CTTGTGCTCGTTGTGCGCCGCGGTCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L V L V V A A V L L L V S A E S A L I T
 310 330 350
 CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCCTCA
 Q Q D L A P Q Q R A A P Q Q K R S S P S
 370 390 410
 GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
 E G L C P P G H H I S E D G R D C I S C
 430 450 470
 AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
 K Y G Q D Y S T H W N D L L F C L R C T
 490 510 530
 AGGTGTGATTACAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
 R C D S G E V E L S P C T T T R N T V C
 550 570 590
 CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
 Q C E E G T F R E E D S P E M C R K C R
 610 630 650
 ACAGGGTGTCCCAGAGGGATGGTCAAGGTGCGGTGATTGTACACCCTGGAGTGACATCGAA
 T G C P R G M V K V G D C T P W S D I E
 670 690 710
 TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C V H K E S G I I I G V T V A A V V L I
 730 750 770
 GTGGCTGTGTTTGTGTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G
 790 810 830
 ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
 I C S G G G G D P E R V D R S S Q R P G

FIG.1A

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850 870 890
 GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
 A E D N V L N E I V S I L Q P T Q V P E
 910 930 950
 CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
 Q E M E V Q E P A E P T G V N M L S P G
 970 990 1010
 GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
 E S E H L L E P A E A E R S Q R R R L L
 1030 1050 1070
 GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
 V P A N E G D P T E T L R Q C F D D F A
 1090 1110 1130
 GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
 D L V P F D S W E P L M R K L G L M D N
 1150 1170 1190
 GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
 E I K V A K A E A A G H R D T L Y T M L
 1210 1230 1250
 ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
 I K W V N K T G R D A S V H T L L D A L
 1270 1290 1310
 GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
 E T L G E R L A K Q K I E D H L L S S G
 1330 1350 1370
 AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
 K F M Y L E G N A D S A M S *
 1390 1410 1430
 GGAAGTGAGACCTTCCCTGGTTTACCTTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
 1450 1470 1490
 AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAACTCTCCCATCCAACA
 1510 1530 1550
 TCACCCAGTGATGGAACATCCTGTAACCTTTTCACTGCACTTGGCATTATTTTATAAGC
 1570 1590
 TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAA

FIG. 1B

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FIG. 2A

149	-	-	-	-	-	C E H G I	I - - K E C	- - - T L	T S N T K	C K E	- -	h Fas protein
161	K Q N T	V C T	C H A	G F F	L R E N	E C V S C	S N C K K S	L E C T K	L P Q	I E	-	h TNFR I protei
158	R D T D	C G T C	L P G F Y	E H G D G	C V S C P	T S T L G	- S C P E R	C A V C G	D R 3	p r o t e i n		
163	G M V K	V G D C	T P -	- W S D I	E C V -	- - - -	- - - H K	E S G I I	I G	H L Y B X 8 8 X X p r o t e i		

	h Fas protein	h TNFR I Protein	DR3 protein	HLYBX88XXprotei
168	-	-	-	-
201	-	-	-	-
197	-	-	-	-
198	-	-	-	-

[illegible]

	h Fas protein	h TNFR I Protein	DR3 protein	HLYBX88XXprotei
213	-	-	-	-
219	-	-	-	-
225	-	-	-	-
231	-	-	-	-
237	-	-	-	-
243	-	-	-	-
249	-	-	-	-
255	-	-	-	-
261	-	-	-	-
267	-	-	-	-
273	-	-	-	-
279	-	-	-	-
285	-	-	-	-
291	-	-	-	-
297	-	-	-	-
303	-	-	-	-
309	-	-	-	-
315	-	-	-	-
321	-	-	-	-
327	-	-	-	-
333	-	-	-	-
339	-	-	-	-
345	-	-	-	-
351	-	-	-	-
357	-	-	-	-
363	-	-	-	-
369	-	-	-	-
375	-	-	-	-
381	-	-	-	-
387	-	-	-	-
393	-	-	-	-
399	-	-	-	-
405	-	-	-	-
411	-	-	-	-
417	-	-	-	-
423	-	-	-	-
429	-	-	-	-
435	-	-	-	-
441	-	-	-	-
447	-	-	-	-
453	-	-	-	-
459	-	-	-	-
465	-	-	-	-
471	-	-	-	-
477	-	-	-	-
483	-	-	-	-
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495	-	-	-	-
501	-	-	-	-
507	-	-	-	-
513	-	-	-	-
519	-	-	-	-
525	-	-	-	-
531	-	-	-	-
537	-	-	-	-
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555	-	-	-	-
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567	-	-	-	-
573	-	-	-	-
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585	-	-	-	-
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597	-	-	-	-
603	-	-	-	-
609	-	-	-	-
615	-	-	-	-
621	-	-	-	-
627	-	-	-	-
633	-	-	-	-
639	-	-	-	-
645	-	-	-	-
651	-	-	-	-
657	-	-	-	-
663	-	-	-	-
669	-	-	-	-
675	-	-	-	-
681	-	-	-	-
687	-	-	-	-
693	-	-	-	-
699	-	-	-	-
705	-	-	-	-
711	-	-	-	-
717	-	-	-	-
723	-	-	-	-
729	-	-	-	-
735	-	-	-	-
741	-	-	-	-
747	-	-	-	-
753	-	-	-	-
759	-	-	-	-
765	-	-	-	-
771	-	-	-	-
777	-	-	-	-
783	-	-	-	-
789	-	-	-	-
795	-	-	-	-
801	-	-	-	-
807	-	-	-	-
813	-	-		

213	-	-	-	-	-	P T L N P E T V A I N L - - S D V D L S K Y I T T I A G V M h Fas protein
318	Y Q G A D P I L A T A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A h TNFR I Protein					
305	S R A L G P A A P T L S P - - - - E S P A G S P A M L Q P G P Q DR3 protein					
283	-	-	-	-	L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q HLYBX88XXprotein	4

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FIG. 2B

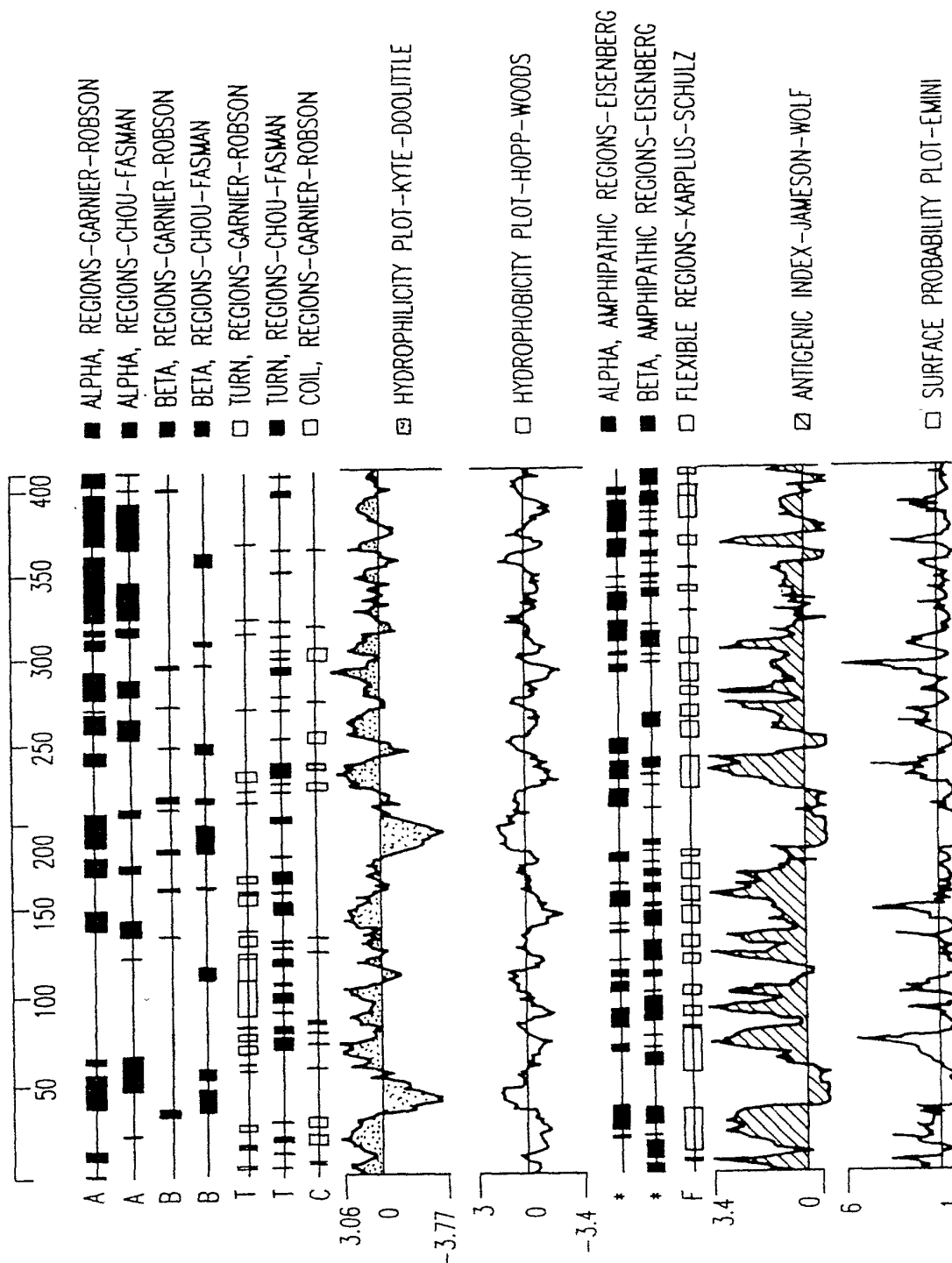
Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exact

FIG. 2C

Appl. No. To be assigned; Group Art Unit: To be assigned
(Divisional of Appl. No. 09/042, 583; Filed: March 17, 1998)
Dkt. No. 1488.131000A/EKS/EJH;
Inventors: NI et al.; Tel: 202/371-2600
Title: Death Domain Containing Receptor 5

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FIG. 3



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HAPBU13R

1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG

HSBBU76R

1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTT CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT

FIG.4

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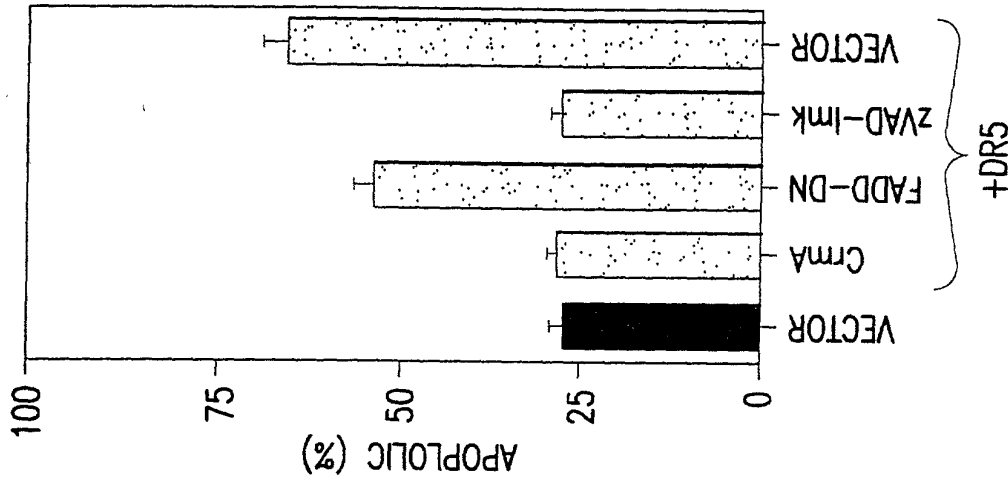


FIG. 5C

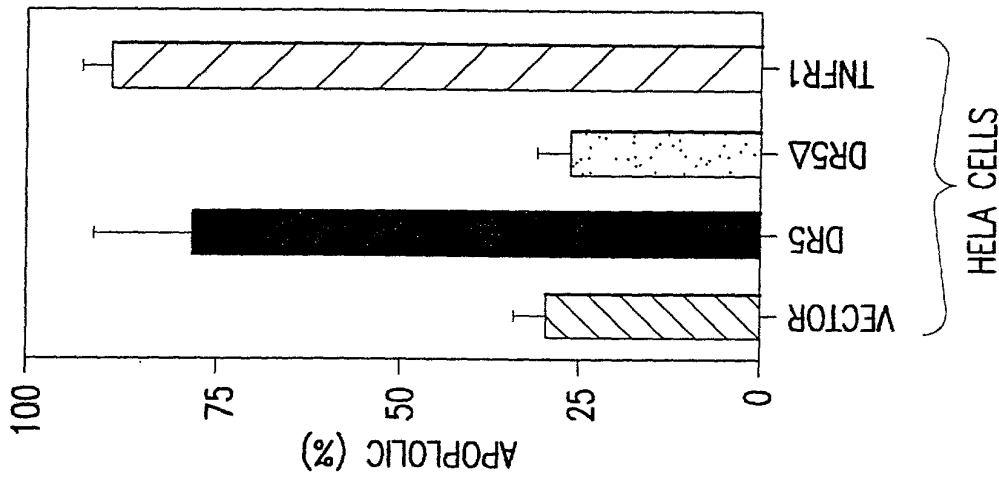


FIG. 5B

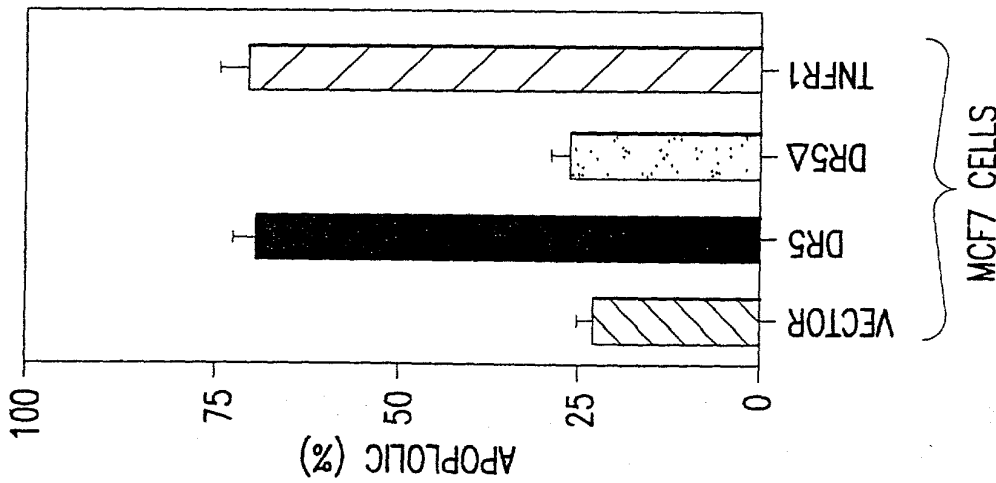


FIG. 5A

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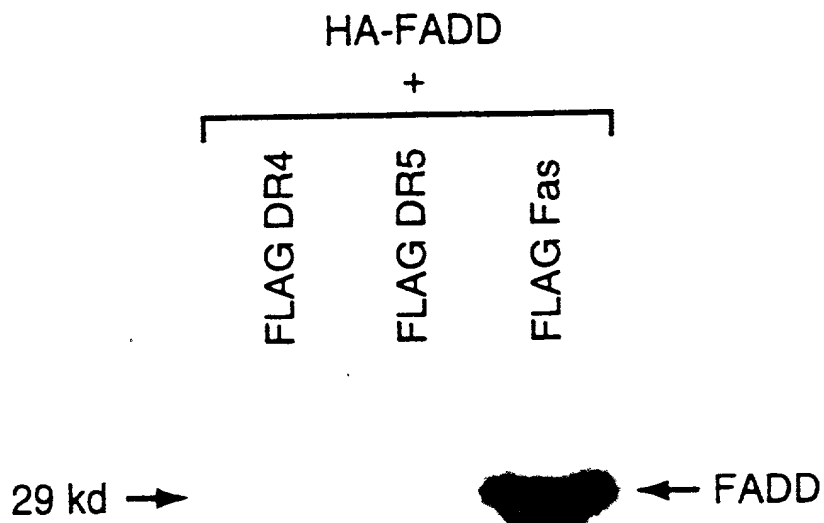
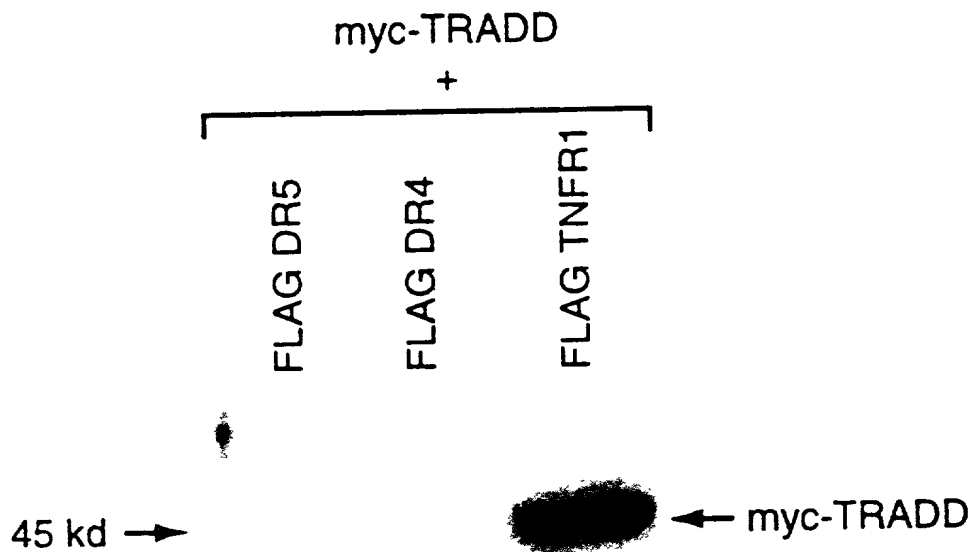


FIG.5D



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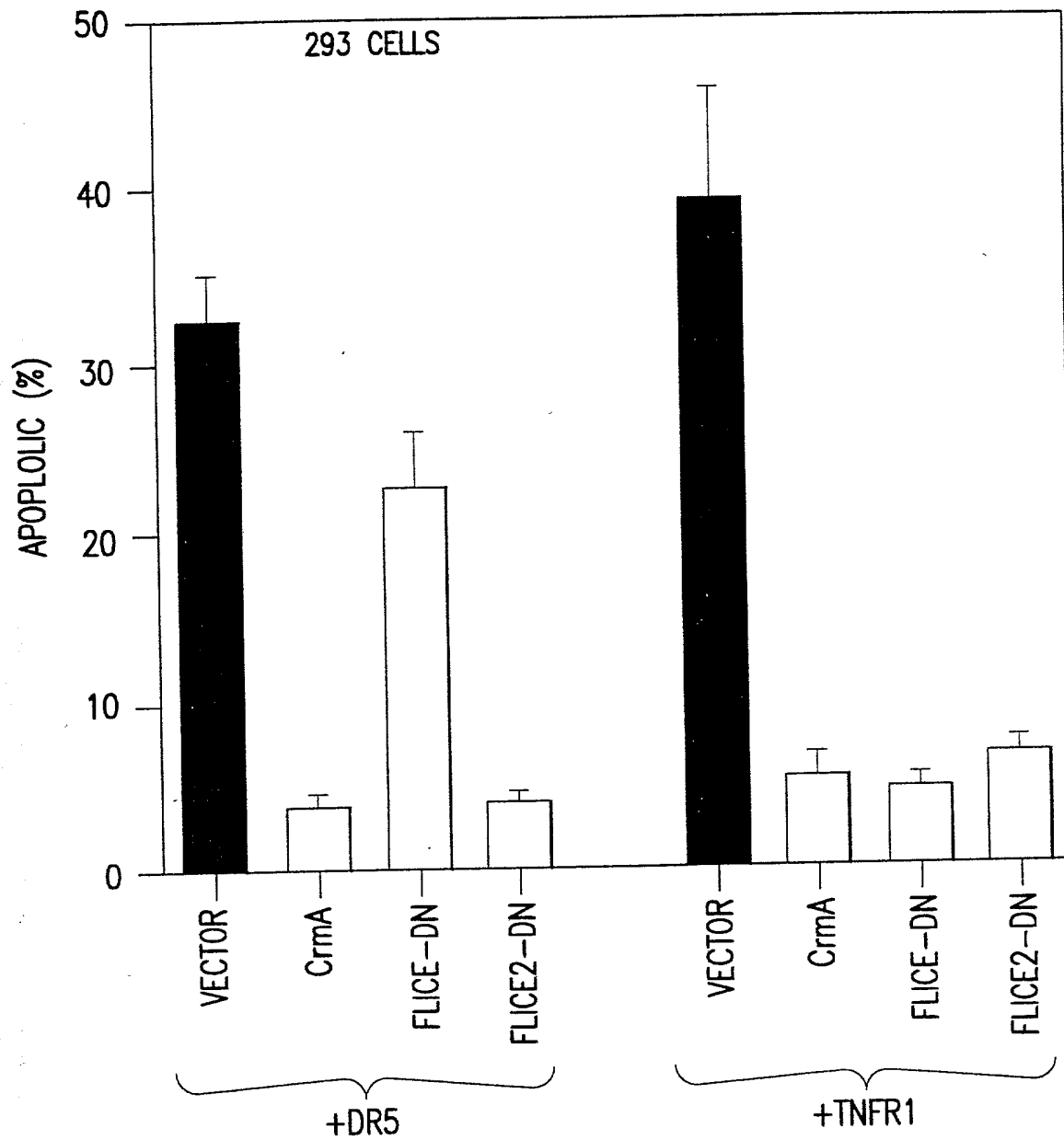


FIG. 5E

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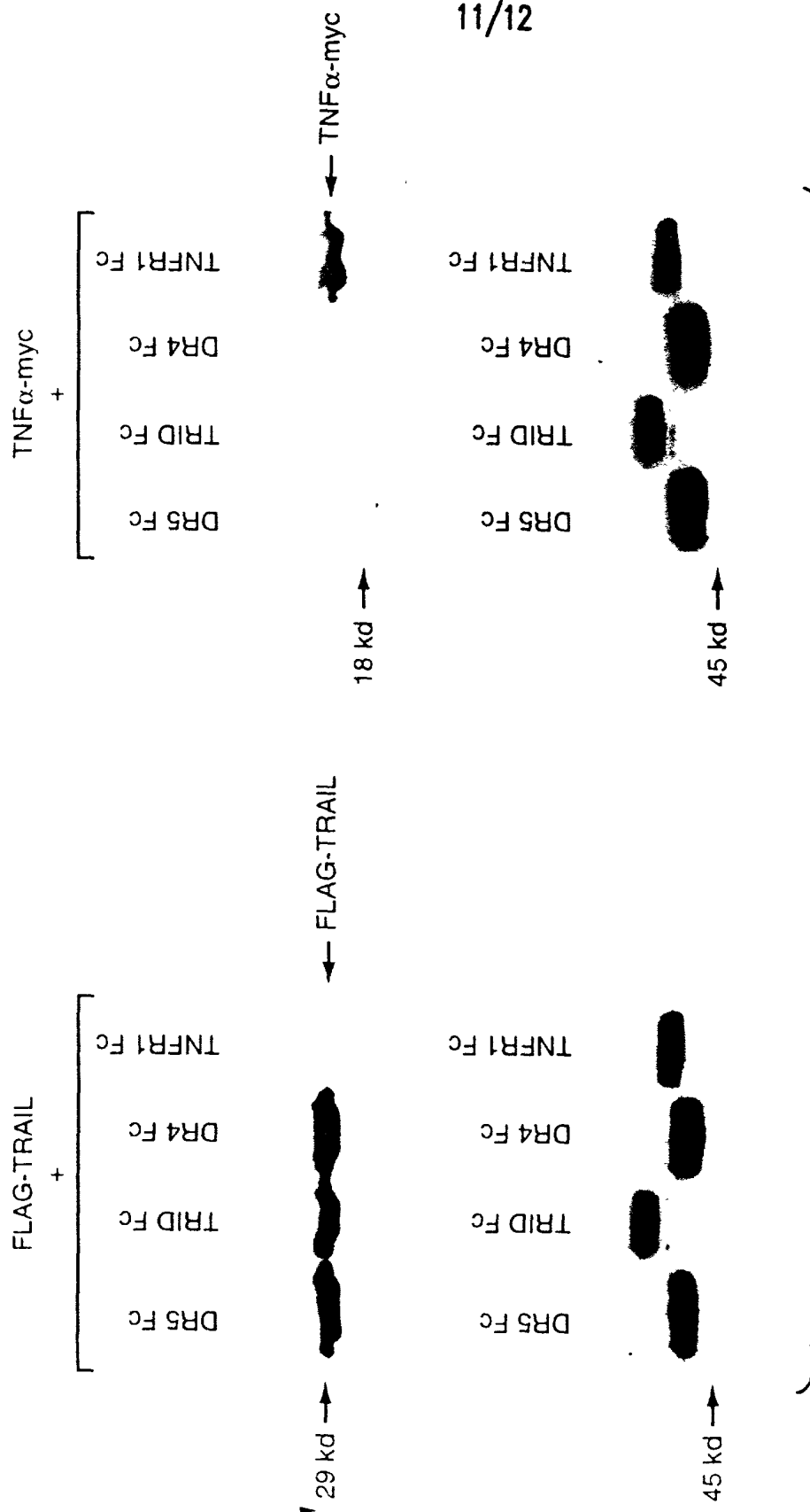


FIG. 6A

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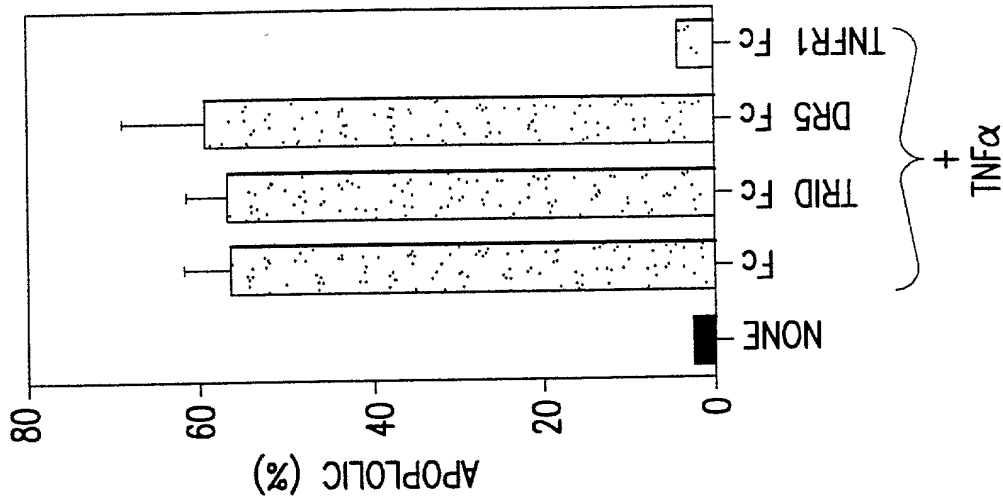


FIG. 6C

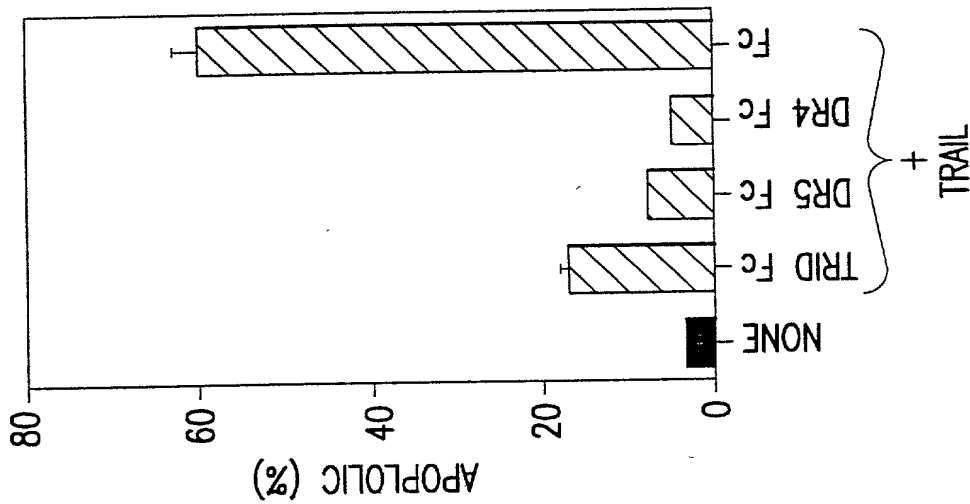


FIG. 6B

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